REMARKS

Currently pending in the application are claims 23 through 42.

The Examiner has asked for a new oath which references the parent serial number, and it is provided in the appendix following this amendment.

In response to the Examiner's comments regarding the sequence listing, the SEQ ID NOs have been added to the specification at page 9, lines 10-11 and at page 9 in reference to Figure 8.

The Examiner's suggestion that a comma be inserted before "wherein" in claim 27 is complied with in this amendment. The Examiner has also suggested that "isolated regulatory" be inserted before "nucleotide" in claim 40. It is believed the Examiner is referring to claim 41, and it has been so amended.

The term "isolated" has been inserted into claims 24-26, and thus it is believed the section 101 rejection is overcome.

Claims 30, 33-37 and 40 are rejected under section 112, second paragraph as indefinite in reciting in the independent claims, 30 and 33 "a nucleotide sequence that prevents the development of plant male tissues." The Applicant has replaced this language with recitation that the nucleotide sequence "disrupts male tissue function." The specification describes disruption of male tissue function specifically at page 17, lines 14-17, and provides examples of same beginning at page 17, line 17 through page 19, line 15. Thus it is believed the language has been clarified.

Claims 23-42 are rejected under section 112, first paragraph as enabled for an isolated regulatory sequence of SEQ ID NO: 1 or 2, but not for regulatory regions from 1 to 1311, or 1155 to 1311, or 1179 to 1208 or 1239 to 1278 or any fragment thereof. The Examiner says no regions necessary for regulatory activity are disclosed or evaluated for these sequences. The Examiner's attention is directed to Example 5, in which data is presented that demonstrates that these regions are those essential for regulatory activity. The regions are described in relations to the TATA box of the sequence set forth. In the parent application, the Examiner had requested they instead recite the corresponding bases of the sequence, and they now so recite.

This Example shows that a series of 5' as well as 3' deletions to the promoter sequence. Figure 8 shows fifteen deletions that were carried out. Linker scanning

mutations were generated by site-directed mutagenesis. The derivatives were fused to a luciferase reporter gene and expression measured following transformation of plant tissue. Figure 9 shows luciferase activities normalized to GUS as a percent of the wild type full length sequence, and Figure 10 shows luciferase activity plotted against the linker scanning mutant of the MS45 promoter fused to the luciferase promoter. As a result four regions were to be essential for male tissue expression regulation; those sequences corresponding to base 1 to base 1311; those corresponding to bases 1155 to base 1311; those corresponding to 1179 to base 1208; and those from base 1239 to base 1278 of SEQ ID NOs: 1 or 2. See the specification, starting at page 31, line 10 and continuing to page 33, line 6.

The inventors have contributed to the state of the art by identifying the promoter of MS45, and those fragments which are essential to retaining regulatory activity. They have demonstrated regions that are of particular importance, providing four examples of such sequences. Further, these claims require that the fragments involved are essential for regulatory activity. The specification provides an outline for such a determination in discussion of functional analysis, such as in Example 5, by observing reporter gene expression in male tissue and reduction or absence of that expression. That this is common practice is evidenced by discussion in such publications as U.S. Patent No. 5,352,605 which shows essential regions of the CaMV 19S and 35S promoters. In Example 5, the inventors show how this was accomplished in specific examples, using the luciferase reporter gene. The inventors have outlined the specifics of how they obtained such fragments and tested them to ascertain that they were essential for regulatory activity. It is a straightforward test to determine if sequences retain regulatory activity.

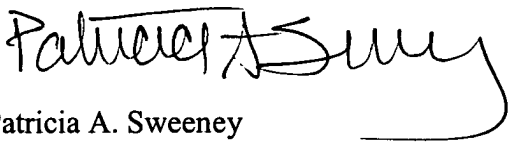
The Examiner also comments that claims to sequences which hybridize or have 75% identity would comprise non-functional elements. However, the claims as amended in the preliminary amendment do not include claims to sequences which hybridize.

Therefore it is believed the section 112 rejection has been overcome, in that the regions recited, fragments of the promoter which retain regulatory activity have been exemplified in the specification.

Claims 32, 38-39 and 41 are rejected under section 102(b) as anticipated by Cigan et al., which teaches an isolated anther-specific promoter of the 5126 gene. The rejection is respectfully traversed. There rejection does not state the sequences are the same and indeed they are not. The claim is not to any fragment – it is to a fragment of SEQ ID NOs: 1 or 2. Further, independent claim 32 is to a fragment which retains the function recited. The claim is amended to clarify that the fragment is one "essential for" regulatory activity. Thus, it is not any fragment of the sequence, but fragments that retain the function of being essential regulatory activity.

For these reasons it is respectfully requested that reconsideration and allowance of the claims be granted. In the event the Examiner believes there are issues remaining to be resolved regarding allowance of the claims, a telephonic interview is requested.

Respectfully submitted,



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